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A method and system for quantifying the relative abundance of gene transcripts in a biological specimen. One embodiment of the mode generates high-droughput sequence-specific analysis of multiple RNAs or their corresponding cDNAs (gene transcript imaging analysis). Another embodiment of the method produces a gene transcript imaging analysis by the use of high-droughput cDNAs equence analysis. In addition, the gene transcript imaging can be used to detect or diagnose a particular biological state, disease, or condition which is correlated to the relative abundance of gene transcripts in agive need 10 production of cells. The invention provides a method for comparing the gene transcript image analysis from two or more different biological speciments in order to distinguish between the two specimens and identify once or more genes which are differentially expressed between the two specimes.